

## **RAW SEQUENCE LISTING**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/510,508  
Source: PCT  
Date Processed by STIC: 10/16/04

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PCT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/510,508

DATE: 10/16/2004

TIME: 09:07:20

Input Set : A:\2543-1-038PCTUS - Seq List.txt  
 Output Set: N:\CRF4\10162004\J510508.raw

3 <110> APPLICANT: Terrett, Jonathan A  
 5 <120> TITLE OF INVENTION: Protein Involved in Cancer  
 7 <130> FILE REFERENCE: 2543-1-038PCT/US  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/510,508  
 C--> 10 <141> CURRENT FILING DATE: 2004-10-07  
 12 <150> PRIOR APPLICATION NUMBER: GB0208332.7  
 13 <151> PRIOR FILING DATE: 2002-04-11  
 15 <150> PRIOR APPLICATION NUMBER: GB0229875.0  
 16 <151> PRIOR FILING DATE: 2002-12-21  
 18 <160> NUMBER OF SEQ ID NOS: 6  
 20 <170> SOFTWARE: PatentIn version 3.1  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 1212  
 24 <212> TYPE: PRT  
 25 <213> ORGANISM: Homo sapiens  
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 30 1 5 10 15  
 32 Gly Val Gly Glu Thr Pro Ser Ala Ala Ala Leu Ala Ala Ala Arg Val  
 33 20 25 30  
 35 Glu Leu Pro Gly Thr Ala Val Pro Ser Val Pro Glu Asp Ala Ala Pro  
 36 35 40 45  
 38 Ala Ser Arg Asp Gly Gly Val Arg Asp Glu Gly Pro Ala Ala Ala  
 39 50 55 60  
 41 Gly Asp Gly Leu Gly Arg Pro Leu Gly Pro Thr Pro Ser Gln Ser Arg  
 42 65 70 75 80  
 44 Phe Gln Val Asp Leu Val Ser Glu Asn Ala Gly Arg Ala Ala Ala  
 45 85 90 95  
 47 Ala Ala Ala Ala Ala Ala Ala Ala Ala Gly Ala Gly Ala Gly  
 48 100 105 110  
 50 Ala Lys Gln Thr Pro Ala Asp Gly Glu Ala Ser Gly Glu Ser Glu Pro  
 51 115 120 125  
 53 Ala Lys Gly Ser Glu Glu Ala Lys Gly Arg Phe Arg Val Asn Phe Val  
 54 130 135 140  
 56 Asp Pro Ala Ala Ser Ser Ala Glu Asp Ser Leu Ser Asp Ala Ala  
 57 145 150 155 160  
 59 Gly Val Gly Val Asp Gly Pro Asn Val Ser Phe Gln Asn Gly Gly Asp  
 60 165 170 175  
 62 Thr Val Leu Ser Glu Gly Ser Ser Leu His Ser Gly Gly Gly Gly  
 63 180 185 190  
 65 Ser Gly His His Gln His Tyr Tyr Tyr Asp Thr His Thr Asn Thr Tyr  
 66 195 200 205  
 68 Tyr Leu Arg Thr Phe Gly His Asn Thr Met Asp Ala Val Pro Arg Ile

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71	Asp His Tyr Arg His Thr Ala Ala Gln Leu Gly Glu Lys Leu Leu Arg			
72	225	230	235	240
74	Pro Ser Leu Ala Glu Leu His Asp Glu Leu Glu Lys Glu Pro Phe Glu			
75	245	250	255	
77	Asp Gly Phe Ala Asn Gly Glu Glu Ser Thr Pro Thr Arg Asp Ala Val			
78	260	265	270	
80	Val Thr Tyr Thr Ala Glu Ser Lys Gly Val Val Lys Phe Gly Trp Ile			
81	275	280	285	
83	Lys Gly Val Leu Val Arg Cys Met Leu Asn Ile Trp Gly Val Met Leu			
84	290	295	300	
86	Phe Ile Arg Leu Ser Trp Ile Val Gly Gln Ala Gly Ile Gly Leu Ser			
87	305	310	315	320
89	Val Leu Val Ile Met Met Ala Thr Val Val Thr Thr Ile Thr Gly Leu			
90	325	330	335	
92	Ser Thr Ser Ala Ile Ala Thr Asn Gly Phe Val Arg Gly Gly Ala			
93	340	345	350	
95	Tyr Tyr Leu Ile Ser Arg Ser Leu Gly Pro Glu Phe Gly Gly Ala Ile			
96	355	360	365	
98	Gly Leu Ile Phe Ala Phe Ala Asn Ala Val Ala Val Ala Met Tyr Val			
99	370	375	380	
101	Val Gly Phe Ala Glu Thr Val Val Glu Leu Leu Lys Glu His Ser Ile			
102	385	390	395	400
104	Leu Met Ile Asp Glu Ile Asn Asp Ile Arg Ile Ile Gly Ala Ile Thr			
105	405	410	415	
107	Val Val Ile Leu Leu Gly Ile Ser Val Ala Gly Met Glu Trp Glu Ala			
108	420	425	430	
110	Lys Ala Gln Ile Val Leu Leu Val Ile Leu Leu Leu Ala Ile Gly Asp			
111	435	440	445	
113	Phe Val Ile Gly Thr Phe Ile Pro Leu Glu Ser Lys Lys Pro Lys Gly			
114	450	455	460	
116	Phe Phe Gly Tyr Lys Ser Glu Ile Phe Asn Glu Asn Phe Gly Pro Asp			
117	465	470	475	480
119	Phe Arg Glu Glu Glu Thr Phe Phe Ser Val Phe Ala Ile Phe Phe Pro			
120	485	490	495	
122	Ala Ala Thr Gly Ile Leu Ala Gly Ala Asn Ile Ser Gly Asp Leu Ala			
123	500	505	510	
125	Asp Pro Gln Ser Ala Ile Pro Lys Gly Thr Leu Leu Ala Ile Leu Ile			
126	515	520	525	
128	Thr Thr Leu Val Tyr Val Gly Ile Ala Val Ser Val Gly Ser Cys Val			
129	530	535	540	
131	Val Arg Asp Ala Thr Gly Asn Val Asn Asp Thr Ile Val Thr Glu Leu			
132	545	550	555	560
134	Thr Asn Cys Thr Ser Ala Ala Cys Lys Leu Asn Phe Asp Phe Ser Ser			
135	565	570	575	
137	Cys Glu Ser Ser Pro Cys Ser Tyr Gly Leu Met Asn Asn Phe Gln Val			
138	580	585	590	
140	Met Ser Met Val Ser Gly Phe Thr Pro Leu Ile Ser Ala Gly Ile Phe			
141	595	600	605	

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143 Ser Ala Thr Leu Ser Ser Ala Leu Ala Ser Leu Val Ser Ala Pro Lys  
144 610 615 620  
146 Ile Phe Gln Ala Leu Cys Lys Asp Asn Ile Tyr Pro Ala Phe Gln Met  
147 625 630 635 640  
149 Phe Ala Lys Gly Tyr Gly Lys Asn Asn Glu Pro Leu Arg Gly Tyr Ile  
150 645 650 655  
152 Leu Thr Phe Leu Ile Ala Leu Gly Phe Ile Leu Ile Ala Glu Leu Asn  
153 660 665 670  
155 Val Ile Ala Pro Ile Ile Ser Asn Phe Phe Leu Ala Ser Tyr Ala Leu  
156 675 680 685  
158 Ile Asn Phe Ser Val Phe His Ala Ser Leu Ala Lys Ser Pro Gly Trp  
159 690 695 700  
161 Arg Pro Ala Phe Lys Tyr Tyr Asn Met Trp Ile Ser Leu Leu Gly Ala  
162 705 710 715 720  
164 Ile Leu Cys Cys Ile Val Met Phe Val Ile Asn Trp Trp Ala Ala Leu  
165 725 730 735  
167 Leu Thr Tyr Val Ile Val Leu Gly Leu Tyr Ile Tyr Val Thr Tyr Lys  
168 740 745 750  
170 Lys Pro Asp Val Asn Trp Gly Ser Ser Thr Gln Ala Leu Thr Tyr Leu  
171 755 760 765  
173 Asn Ala Leu Gln His Ser Ile Arg Leu Ser Gly Val Glu Asp His Val  
174 770 775 780  
176 Lys Asn Phe Arg Pro Gln Cys Leu Val Met Thr Gly Ala Pro Asn Ser  
177 785 790 795 800  
179 Arg Pro Ala Leu Leu His Leu Val His Asp Phe Thr Lys Asn Val Gly  
180 805 810 815  
182 Leu Met Ile Cys Gly His Val His Met Gly Pro Arg Arg Gln Ala Met  
183 820 825 830  
185 Lys Glu Met Ser Ile Asp Gln Ala Lys Tyr Gln Arg Trp Leu Ile Lys  
186 835 840 845  
188 Asn Lys Met Lys Ala Phe Tyr Ala Pro Val His Ala Asp Asp Leu Arg  
189 850 855 860  
191 Glu Gly Ala Gln Tyr Leu Met Gln Ala Ala Gly Leu Gly Arg Met Lys  
192 865 870 875 880  
194 Pro Asn Thr Leu Val Leu Gly Phe Lys Lys Asp Trp Leu Gln Ala Asp  
195 885 890 895  
197 Met Arg Asp Val Asp Met Tyr Ile Asn Leu Phe His Asp Ala Phe Asp  
198 900 905 910  
200 Ile Gln Tyr Gly Val Val Val Ile Arg Leu Lys Glu Gly Leu Asp Ile  
201 915 920 925  
203 Ser His Leu Gln Gly Gln Glu Glu Leu Leu Ser Ser Gln Glu Lys Ser  
204 930 935 940  
206 Pro Gly Thr Lys Asp Val Val Val Ser Val Glu Tyr Ser Lys Lys Ser  
207 945 950 955 960  
209 Asp Leu Asp Thr Ser Lys Pro Leu Ser Glu Lys Pro Ile Thr His Lys  
210 965 970 975  
212 Val Glu Glu Glu Asp Gly Lys Thr Ala Thr Gln Pro Leu Leu Lys Lys  
213 980 985 990  
215 Glu Ser Lys Gly Pro Ile Val Pro Leu Asn Val Ala Asp Gln Lys Leu

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Output Set: N:\CRF4\10162004\J510508.raw

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218	Leu Glu Ala Ser Thr Gln Phe Gln Lys Lys Gln Gly Lys Asn Thr		
219	1010	1015	1020
221	Ile Asp Val Trp Trp Leu Phe Asp Asp Gly Gly Leu Thr Leu Leu		
222	1025	1030	1035
224	Ile Pro Tyr Leu Leu Thr Thr Lys Lys Lys Trp Lys Asp Cys Lys		
225	1040	1045	1050
227	Ile Arg Val Phe Ile Gly Gly Lys Ile Asn Arg Ile Asp His Asp		
228	1055	1060	1065
230	Arg Arg Ala Met Ala Thr Leu Leu Ser Lys Phe Arg Ile Asp Phe		
231	1070	1075	1080
233	Ser Asp Ile Met Val Leu Gly Asp Ile Asn Thr Lys Pro Lys Lys		
234	1085	1090	1095
236	Glu Asn Ile Ile Ala Phe Glu Glu Ile Ile Glu Pro Tyr Arg Leu		
237	1100	1105	1110
239	His Glu Asp Asp Lys Glu Gln Asp Ile Ala Asp Lys Met Lys Glu		
240	1115	1120	1125
242	Asp Glu Pro Trp Arg Ile Thr Asp Asn Glu Leu Glu Leu Tyr Lys		
243	1130	1135	1140
245	Thr Lys Thr Tyr Arg Gln Ile Arg Leu Asn Glu Leu Leu Lys Glu		
246	1145	1150	1155
248	His Ser Ser Thr Ala Asn Ile Ile Val Met Ser Leu Pro Val Ala		
249	1160	1165	1170
251	Arg Lys Gly Ala Val Ser Ser Ala Leu Tyr Met Ala Trp Leu Glu		
252	1175	1180	1185
254	Ala Leu Ser Lys Asp Leu Pro Pro Ile Leu Leu Val Arg Gly Asn		
255	1190	1195	1200
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258	1205	1210	
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261	<211> LENGTH: 4098		
262	<212> TYPE: DNA		
263	<213> ORGANISM: Homo sapiens		

W--> 264 <400> SEQUENCE: 2

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267 ctccacctggat cttgc

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269 agacgtccccggc cggggcc  
271 cggggggggatc atccggg

271	ccggcgcccc	cctccggcgcc	ccgggactgg	ccggggatcg	ggagacgcgg	tcagccgtg	240
273	cgctggccgc	agccagggtg	gaactgcccgg	gcacggctgt	gccctcggtg	ccggaggatg	300
275	ctgcgccccgc	gagccgggac	ggcggcgggg	tccgcgatga	gggcccccg	gcggccgggg	360
277	acgggctggg	cagacccttg	gggcccaccc	cgagccagag	ccgtttccag	gtggacctgg	420
279	tttccgagaa	cgccgggggg	gccgcgtgctg	cgccgggggc	ggggcggcg	gcagccggcg	480
281	cggctgggtgc	tggggcgggg	gccaagcaga	ccccccgcgg	cggggaaagcc	agcggcgaga	540
283	gcgagccagc	taaaggcagc	gaggaagcca	agggccgctt	ccgcgtgaac	ttcggtggacc	600
285	cagctgcctc	ctcgctcggt	gaagacagcc	tgtcagatgc	tgccggggtc	ggagtgcacg	660
287	ggcccaacgt	gagcttccag	aacggcgggg	acacgggtct	gagcgagggc	agcagacctgc	720
289	actccggcgg	cggcggcggc	agtgggcacc	accagcacta	ctattatgtat	acccacacca	780
291	acaccta	cctgcgcacc	ttcggccaca	acaccatgga	cgctgtgccc	aggatcgatc	840
293	actaccggca	cacagcogcg	cagctggcg	agaagctgct	ccggccttagc	ctggcggagc	900

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299	gctggatcaa	gggtgtatta	gtacgttta	tgttaaacat	ttgggggtgt	atgtttca	1080
301	tttagattgtc	atggattgt	ggtcaagct	gaataggct	atcagtctt	gtaataatga	1140
303	tggccactgt	tgtgacaact	atcacaggat	tgtctacttc	agcaaatgca	actaatggat	1200
305	ttgtaagagg	aggaggagca	tattatttaa	tatctagaag	tctagggcca	gaatttggtg	1260
307	gtgcaattgg	tctaatttcc	gcctttgcca	acgcgttgc	agttgctatg	tatgtgggt	1320
309	gatttgcaga	aaccgtgg	gagttgctt	aggaacattc	catactttag	atagatgaaa	1380
311	tcaatgatat	ccgaattatt	ggagccatta	cagtcgtgat	tcttttaggt	atctcagtag	1440
313	ctggaatgga	gtggaaagca	aaagctcaga	ttgttcttt	ggtgatccta	cttcttgcta	1500
315	ttgggtgatt	cgtcatagga	acatttatcc	cactggagag	caagaaggcca	aaagggttt	1560
317	ttggttataa	atctgaaata	ttaatgaga	actttgggc	cgattttcga	gaggaagaga	1620
319	cttcttttc	tgtatttgcc	atcttttcc	ctgctgcaac	tggtattctg	gctggagcaa	1680
321	atatctcagg	tgatcttgc	gatcctcagt	cagccatacc	caaaggaaaca	ctcctagcca	1740
323	tttaatttac	tacattgg	tacgttaggaa	ttgcagtatc	tgttaggtct	tgtgttgg	1800
325	gagatgccac	tggaaacgtt	aatgacacta	tcgtacacaga	gctaacaac	tgtacttctg	1860
327	cagcctgcaa	attaaactt	gattttcat	cttgcgaaag	cagtcctgt	tcctatggcc	1920
329	taatgaacaa	cttccaggta	atgagttatgg	tgtcaggatt	tacaccacta	atttctgcag	1980
331	gtatattttc	agccactt	tcttcagcat	tagcatccct	agtgagtct	ccccaaatat	2040
333	ttcaggctct	atgtaaggac	aacatctacc	cagcttcca	gatgtttct	aaaggttatg	2100
335	ggaaaaataa	tgaacctt	cgtggctaca	tcttaacatt	cttaattgca	cttggattca	2160
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339	atgcatttgc	caattttca	gtattccatg	catcaattgc	aaaatctcca	ggatggcg	2280
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351	atcttgc	tgatttcaca	aaaaatgtt	gtttgatgt	ctgtggccat	gtacatatgg	2640
353	gtcctcgaag	acaagccat	aaagagatgt	ccatcgatca	agccaaatat	cagcgatgg	2700
355	ttattaaagaa	caaaatgaaag	gcattttatg	ctccagtaca	tgcagatgac	ttgagagaag	2760
357	gtgcacagta	tttgcgtc	gtgcgtgg	ttggcgtat	gaagccaaac	acacttgtcc	2820
359	ttggatttaa	gaaagattgg	ttgcaagcag	atatgaggga	tgtggatatg	tatataaaact	2880
361	tatttgc	tgcatttgc	atacaatatg	gagtagtgg	tattcgctt	aaagaagg	2940
363	tggatataatc	tcatcttca	ggacaagaag	aattattgtc	atcacaagag	aaatctctg	3000
365	gcaccaagga	tgtggtagta	agtgtggat	atagaaaaaa	gtccgattta	gataacttcca	3060
367	aaccactca	tgaaaaacca	attacacaca	aagtgg	agaggatgg	aagactgca	3120
369	ctcaaccact	gttggaaaaaa	gaatccaaag	gccctattgt	gcctttaat	gtagctgacc	3180
371	aaaagttct	tgaagctgt	acacagttt	agaaaaaaca	aggaaagaat	actattgtat	3240
373	tctgggtgg	ttttgatgt	ggagggtt	cattattgt	accttac	ctgacgacca	3300
375	agaaaaatg	gaaagactgt	agatcagag	tattcattgg	tggaaagata	aacagaatag	3360
377	accatgaccg	gagaggcgt	gtacttt	ttagcaagtt	ccggatagac	ttttctgata	3420
379	tcatgg	aggatatac	aatacc	caaagaaaga	aatattata	gctttgagg	3480
381	aaatcattga	gccatacaga	cttcatgaag	atgataaaga	gcaagatatt	gcagataaaa	3540
383	tgaaagaaga	tgaaccatgg	cgaataacag	ataatgagct	tgaactttat	aagaccaaga	3600
385	cataccggca	gatcagg	tttgcgtt	taaaggaaca	ttcaagcaca	gctaatatta	3660
387	ttgtcatgag	tctcc	gtacggaaaag	gtgcgtgt	tagtgc	tacatggcat	3720
389	ggttagaagc	tctatctaag	gac	caattctt	agttcg	tttgggg aatcatcaga	3780
391	gtgtcatttac	tttctattca	taaatgtt	atacagtgg	cagcccttca	gaatggact	3840

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:264 M:283 W: Missing Blank Line separator, <400> field identifier  
L:407 M:283 W: Missing Blank Line separator, <220> field identifier  
L:409 M:283 W: Missing Blank Line separator, <400> field identifier  
L:416 M:283 W: Missing Blank Line separator, <220> field identifier  
L:418 M:283 W: Missing Blank Line separator, <400> field identifier  
L:425 M:283 W: Missing Blank Line separator, <220> field identifier  
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